

Preliminary Amendment
In re: Preben LEXOW
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REMARKS

The accompanying amendments are being made to eliminate multiple dependencies in the claims, and place the Abstract in better U.S. form.

RESPECTFULLY SUBMITTED,					
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Attachments: Version of amended claims to show changes made and Abstract

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Amended Claims: Version to show changes made

8. (Amended) A method as claimed in [any one of claims 1 to 7] claim 1, 2 or 3 wherein said fragments are each between 8 and 25 bases in length.

9. (Amended) A method as claimed in [any one of claims 1 to 8] claim 1, 2 or 3 wherein n is at least 10.

10. (Amended) A method of synthesizing a double stranded nucleic acid molecule comprising at least the steps of:

- 1) generating fragment chains according to the method defined in [any one of claims 1 to 9] claim 1, 2 or 3;
- 2) optionally generating single stranded regions at the end of said fragment chains, wherein said single stranded regions are complementary to the single stranded regions on said fragment chains thus forming complementary pairs of single stranded regions;
- 3) contacting said fragment chains with one another, simultaneously or consecutively, to effect binding of said complementary pairs of single stranded regions.

11. (Amended) A nucleic acid molecule produced according to a method as defined in [any one of claims 1 to 10] claim 1, 2 or 3, or a single stranded nucleic acid molecule thereof.

12. (Amended) A method of identifying the code elements contained in a nucleic acid molecule prepared according to a method as defined in [any one of claims 1 to 10] claim 1, 2 or 3, wherein a probe, carrying a signalling means, specific to one or more code elements, is bound to said nucleic acid molecule and a signal generated by said signalling means is detected, whereby said one or more code elements may be identified.

13. (Amended) A library of fragments as defined in [any one of claims 1 to 12] claim 1, 2 or 3, comprising $(n)_m$ fragments, wherein n is as defined in [any one of claims 1 to 12] claim 1, 2 or 3 and corresponds to the length of chain that said library may produce, and m is an integer

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corresponding to the number of possible code elements or combinations thereof, such that fragments corresponding to all possible code elements for each position in the final chain are provided.

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ABSTRACT

The present invention provides a method of attaching a fragment of a first nucleic acid molecule to a second nucleic acid molecule using adapters to mediate the binding particularly in methods of cloning, methods of producing fragment chains with a readily readable information content, particularly comprising fragments corresponding to code, such as alphanumeric code, the nucleic acid molecules thus produced and kits for performing such methods.